

## SEQUENCE LISTING

<110> Albani, Salvatore

<120> METHODS FOR ISOLATION, QUANTIFICATION,  
CHARACTERIZATION AND MODULATION OF  
ANTIGEN-SPECIFIC T CELLS

<130> 031544.0004.CIP

<140> NOT YET ASSIGNED

<141> 2001-01-09

<150> 60/105,018

<151> 1998-10-20

<150> 09/421,506

<151> 1999-10-19

<150> PCT/US99/2466

<151> 1999-10-19

<160> 24

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide derived from third hyper V  
region of IE molecule Mus musculus

<400> 1

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<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide derived from boe I protein  
of Epstein Barr virus

<400> 2

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09756993-010901

<210> 3  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthesized peptide derived from the hemophilus  
 influenza virus

<400> 3  
 Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys  
 1 5 10 15

<210> 4  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthesized peptide derived from the TCR receptor  
 gene of Mus musculus

<400> 4  
 Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser  
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 Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr  
 20 25 30  
 Arg Leu  
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<210> 5  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthesized peptide derived from the influenza virus

<400> 5  
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<210> 6  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthesized peptide derived from the influenza virus

<400> 6  
 Val Lys Leu Gly Glu Phe Tyr Asn Gln  
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<400> 10  
Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu  
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<210> 11  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
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<210> 12  
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 <213> Homo sapiens

<400> 12  
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<210> 13  
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 <212> PRT  
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<400> 13  
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 1 5

<210> 14  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
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<210> 15  
 <211> 313  
 <212> PRT  
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<220>  
 <223> Fusion constructs with human and bacterial sequences

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<211> 942
<212> DNA
<213> Artificial Sequence
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gaagtgaaag	aagtggcaac	gctgtcctgt	ggtcacaatg	tttctgttga	agagctggca	180
caaactcgca	tctactggca	aaaggagaag	aaaatggtgc	tgactatgat	gtctggggac	240
atgaatatat	ggcccgagta	caagaaccgg	accatctttg	atatcactaa	taacctctcc	300
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tatgaaaaag	acgctttcaa	gcgggaacac	ctgggtgaag	tgacgttatc	agtcaaagct	420
gacttcccta	cacctagtat	atctgcacttt	gaaattccaa	cttctaatat	tagaaggata	480
atttgcctaa	cctctggagg	ttttccagag	cctcacctct	cctggttgga	aaatggagaa	540
gaattaaatg	ccatcaacac	aacaqtttcc	caagatcctg	aaactgaqct	ctatgctqtt	600

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ctagctggaa aaagagagat ggctatcatt acttttaaga atgggtgcaac ttttcaagta 780
gaagtaccag gtagtcaaca tatagattca caaaaaaaaag cgattgaaag gatgaaggat 840
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<210> 17

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 17

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aaccaaagcc tgagtgaagt agtagtattt tggcaggacc aggaaaactt gggttctgaat 180
gaggtatact taggcaaaga gaaatttgac agtggttcatt ccaagtatat gggccgcaca 240
agttttgatt cggacagttg gacctgaga cttcacaatc ttcagatcaa ggacaagggc 300
ttgtatcaat gtatcatcca tcacaaaaag cccacaggaa tgattcgcat ccaccagatg 360
aattctgaac tgtcagtgtc tgctaacttc agtcaacctg aaatagtacc aatttctaata 420
ataacagaaa atgtgtacat aaatttgacc tgctcatcta tacacggtta cccagaacct 480
aagaagatga gtgttttgct aagaaccaag aattcaacta tcgagtatga tgggtattatg 540
cagaaatctc aagataatgt cacagaactg tacgacgttt ccatcagctt gtctgtttca 600
ttccctgatg ttacgagcaa tatgaccatc ttctgtattc tggaaactga caagacgcgg 660
cttttatctt cacctttctc tatagagctt gaggaccctc agcctcccc agaccacgaa 720
ttcggcggtc ccggtggtag cgccacacct caaaatatta ctgatttgtg tgcagaatac 780
cacaacacac aaatacatat gctaaatgat aagatatatt cgtatacaga atctctagct 840
ggaaaaagag agatggctat cattaatttt aagaatgggt caacttttca agtagaagta 900
ccaggtagtc aacatataga ttcacaaaaa aaagcgattg aaaggatgaa ggataccctg 960
aggattgcat atcttactga agctaaagtc gaaaagttat gtgtatggaa taataaaacg 1020
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<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 18

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20           25           30
Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
35           40           45
Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
50           55           60
Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
65           70           75           80
Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
85           90           95

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T050T0-E0695460

Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr  
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 115 120 125  
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn  
 130 135 140  
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro  
 145 150 155 160  
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr  
 165 170 175  
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp  
 180 185 190  
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met  
 195 200 205  
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser  
 210 215 220  
 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu  
 225 230 235 240  
 Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu  
 245 250 255  
 Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile  
 260 265 270  
 Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile  
 275 280 285  
 Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln  
 290 295 300  
 His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu  
 305 310 315 320  
 Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp  
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<210> 19  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptides

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<210> 20  
 <211> 30  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> peptides

<400> 20  
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<210> 21  
 <211> 1095  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fusion constructs with human and bacterial sequences

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 cctgaccaat caggcgagtt tatgtttgac tttgatgggtg atgagatttt ccatgtggat 180  
 atggcaaaaga aggagacggt ctggcgggctt gaagaatttg gacgatttgc cagctttgag 240  
 gctcaagggtg cattggccaa catagctgtg gacaaaacca acctggaaat catgacaaaag 300  
 cgctccaact atactccgat caccaatgta cctccagagg taactgtgct cacgaacagc 360  
 cctgtggaac tgagagagcc caacgtcctc atctgtttca tcgacaagtt caccaccacca 420  
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 aagcactggg agtttgatgc tccaagccct ctcccagaga ctacagagga attcgggtggt 660  
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<210> 22  
 <211> 364  
 <212> PRT  
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<220>  
 <223> Fusion constructs with human and bacterial sequences

<400> 22  
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 20 25 30

T06070-00000000



Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met  
 35 40 45  
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys  
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 Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu  
 65 70 75 80  
 Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu  
 85 90 95  
 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro  
 100 105 110  
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn  
 115 120 125  
 Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val  
 130 135 140  
 Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr  
 145 150 155 160  
 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu  
 165 170 175  
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His  
 180 185 190  
 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro  
 195 200 205  
 Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser  
 210 215 220  
 Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln  
 225 230 235 240  
 Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly  
 245 250 255  
 Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu  
 260 265 270  
 Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr  
 275 280 285  
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys  
 290 295 300  
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp  
 305 310 315 320  
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala  
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<210> 23

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

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 aaacatgagt gtcatttctt caacgggacg gagcgggtgc ggttcttgga cagatacttc 180  
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<211> 285

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

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 35 40 45  
 Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu  
 50 55 60  
 Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr  
 65 70 75 80  
 Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu  
 85 90 95  
 Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr  
 100 105 110  
 Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val  
 115 120 125  
 Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu  
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 Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp  
 145 150 155 160  
 Phe Arg Asn Gly Gln Glu Lys Thr Gly Val Val Ser Thr Gly Leu  
 165 170 175  
 Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr  
 180 185 190  
 Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser  
 195 200 205  
 Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala  
 210 215 220  
 Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu  
 225 230 235 240  
 Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala  
 245 250 255  
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 260 265 270  
 Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His  
 275 280 285

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